

08321-110PC2 SEQLIST.txt

## SEQUENCE LISTING

&lt;110&gt; Thomas Jefferson University

<120> RECOMBINANT ANTIBODIES AND COMPOSITIONS  
AND METHODS FOR MAKING AND USING THE SAME

&lt;130&gt; 08321-110PC2

&lt;150&gt; US 10/461,148

&lt;151&gt; 2003-06-13

&lt;160&gt; 24

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 474

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 1

```

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1 5 10 15
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
20 25 30
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45
Ser Asn Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60
Glu Trp Val Ser Ala Ile Ser Ala Ser Gly His Ser Thr Tyr Leu Ala
65 70 75 80
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110
Tyr Tyr Cys Ala Lys Asp Arg Glu Val Thr Met Ile Val Val Leu Asn
115 120 125
Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Arg Val Thr Val Ser Ser
130 135 140
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
145 150 155 160
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
165 170 175
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
180 185 190
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
195 200 205
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
210 215 220
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225 230 235 240
Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
245 250 255
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
260 265 270
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
275 280 285
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
290 295 300
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305 310 315 320
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu

```

## 08321-110PC2 SEQLIST.txt

```

          325          330          335
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
          340          345          350
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
          355          360          365
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
          370          375          380
Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
          385          390          395
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
          400          405          410
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
          415          420          425
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
          430          435          440
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
          445          450          455
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
          460          465          470

```

<210> 2  
 <211> 234  
 <212> PRT  
 <213> Human

```

<400> 2
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1      5      10      15
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20      25      30
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ala Cys Arg Ala Ser Gln Thr
35      40      45
Ala Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50      55      60
Arg Leu Leu Ile Tyr Asp Thr Ser Asn Arg Ala Thr Gly Ile Pro Ala
65      70      75      80
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser
85      90      95
Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Phe
100      105      110
Asn Trp Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Phe Lys Arg
115      120      125
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130      135      140
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145      150      155      160
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165      170      175
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180      185      190
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195      200      205
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210      215      220
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225      230

```

<210> 3  
 <211> 1557  
 <212> DNA  
 <213> Human

```

<400> 3
atggacacac tttgctccac gctcctgctg ctgaccatcc cttcatgggt cttgtcccaa 60
attaccttga aggagactgg tcctacgctg gtgaaacca cacagaccct cacgctgacc 120

```

## 08321-110PC2 SEQLIST.txt

```

tgcaccttct cgggggttctc actcagcact agtggagtgg gtgtgggctg gatccgtcag 180
ccccaggaa agggcctgga gtgggttaca ctcatattatt gggatgatga taagcggtac 240
agtccatctc tggagaacag ggtcaccatc aggaaggaca cctccaaaaa ccaggtggct 300
cttacaatga cgaacatgga ccctttggac acaggcacat actactgtgc gcacagacaa 360
catatcagca gcttcccgtg gttcgattcc tggggccagg gaaccctggt caccgtctcc 420
tcagcttcca ccaagggccc atcgggtcttc cccctggcgc cctgctccag gagcacctct 480
gggggacacag cggccctggg ctgcctggtc aaggactact tccccgagcc ggtgacgggtg 540
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 600
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcaccag 660
acctacacct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag 720
ctcaaaaccc cacttggtga cacaactcac acatgcccac ggtgcccaga gcccaaactct 780
tgtgacacac ctccccctgt cccacgggtgc ccagagccca aatcttgtga cacacctccc 840
ccgtgcccac ggtgcccaga gcccaaactct tgtgacacac ctcccccatg cccacgggtgc 900
ccagcacctg aactcctggg aggaccgtca gtcttctct tcccccaaaa acccaaggat 960
acccttatga tttcccggac ccctgaggtc acgtgcgtgg tgggtggactg gagccacgaa 1020
gaccccgagg tccagttcaa gtggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1080
aagccgcggg aggagcagtt caacagcacg ttccgtgtgg tcagcgtcct caccgtctctg 1140
caccaggact ggctgaacgg taaggagtac aagtgaagg tctccaacaa agccctccca 1200
gccccatcgc agaaaaccc ctccaaaacc aaaggacagc cccgagaacc acaggtgtac 1260
accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctgggtc 1320
aaaggcttct accccagcga catcgccgtg gagtgggaga gcagcgggca gccggagaa 1380
aactacaaca ccacgcctcc catgctggac tccgacggct ccttcttctc ctacagtaga 1440
ctcaccgtgg acaagagcag gtggcagcag gggaaacatc tctcatgctc cgtgatgcag 1500
gaggctctgc acaaccgctt cagcgagaag agcctctccc tgtctccggg taaatga 1557

```

<210> 4  
 <211> 518  
 <212> PRT  
 <213> Human

<400> 4  
 Met Asp Thr Leu Cys Ser Thr Leu Leu Leu Thr Ile Pro Ser Trp  
 1 5 10 15  
 Val Leu Ser Gln Ile Thr Leu Lys Glu Thr Gly Pro Thr Leu Val Lys  
 20 25 30  
 Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu  
 35 40 45  
 Ser Thr Ser Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys  
 50 55 60  
 Ala Leu Glu Trp Val Thr Leu Ile Tyr Trp Asp Asp Lys Arg Tyr  
 65 70 75 80  
 Ser Pro Ser Leu Glu Asn Arg Val Thr Ile Arg Lys Asp Thr Ser Lys  
 85 90 95  
 Asn Gln Val Ala Leu Thr Met Thr Asn Met Asp Pro Leu Asp Thr Gly  
 100 105 110  
 Thr Tyr Tyr Cys Ala His Arg Gln His Ile Ser Ser Phe Pro Trp Phe  
 115 120 125  
 Asp Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr  
 130 135 140  
 Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser  
 145 150 155 160  
 Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
 165 170 175  
 Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
 180 185 190  
 Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
 195 200 205  
 Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys  
 210 215 220  
 Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu  
 225 230 235 240  
 Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro  
 245 250 255  
 Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu  
 260 265 270  
 Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro  
 275 280 285

## 08321-110PC2 SEQLIST.txt

Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu  
 290 295 300  
 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Lys Pro Lys Asp  
 305 310 315 320  
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 325 330 335  
 Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr Val Asp Gly  
 340 345 350  
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn  
 355 360 365  
 Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
 370 375 380  
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
 385 390 395 400  
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu  
 405 410 415  
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
 420 425 430  
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 435 440 445  
 Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr  
 450 455 460  
 Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
 465 470 475 480  
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys  
 485 490 495  
 Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu  
 500 505 510  
 Ser Leu Ser Pro Gly Lys  
 515

<210> 5  
 <211> 699  
 <212> DNA  
 <213> Human

<400> 5  
 atggcctgga cgtttctcct cctcggcctc ctctctcact gcacaggggc tgtgacgtcc 60  
 tatgtgctga ctcagccacc ctcggtgtca gtggccccag gaaagacggc caggattaac 120  
 tgtgggggaa acaacattga atatagaagt gtgcactggt accagcagaa gtcaggccag 180  
 gccctgttag cggatcatcta tgataatagt gaccggccct cagggatccc tgagcgattc 240  
 tctggttcca aatctgggaa cacggccacc ctgaccatca gcagggtcga agccggggat 300  
 gagggcggact attactgtca ggtgtgggat attagtagtg atgtgtgtctt cggcggaggg 360  
 accaagctga cgtccttagg tcagcccaag gctgccccct cggctcactct gttcccggcc 420  
 tcctctgagg agcttcaagc caacaaggcc acactgggtg gtctcataag tgacttctac 480  
 ccgggagccg tgacagtggc ctggaaggca gatagcagcc ccgtcaaggc gggagtggag 540  
 accaccacac cctccaaaca aagcaacaac aagtacgcgg ccagcagcta tctgagcctg 600  
 acgcctgagc agtggaagtc ccacagaagc tacagctgcc aggtcacgca tgaagggagc 660  
 accgtggaga agacagtggc ccctacagaa tgttcatag 699

<210> 6  
 <211> 232  
 <212> PRT  
 <213> Human

<400> 6  
 Met Ala Trp Thr Val Leu Leu Leu Gly Leu Leu Ser His Cys Thr Gly  
 1 5 10 15  
 Ser Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala  
 20 25 30  
 Pro Gly Lys Thr Ala Arg Ile Asn Cys Gly Gly Asn Asn Ile Glu Tyr  
 35 40 45  
 Arg Ser Val His Trp Tyr Gln Lys Ser Gly Gln Ala Pro Val Ala  
 50 55 60  
 Val Ile Tyr Asp Asn Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe  
 65 70 75 80

## 08321-110PC2 SEQLIST.txt

Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val  
 85 90 95  
 Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ile Ser  
 100 105 110  
 Ser Asp Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln  
 115 120 125  
 Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu  
 130 135 140  
 Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr  
 145 150 155 160  
 Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys  
 165 170 175  
 Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr  
 180 185 190  
 Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His  
 195 200 205  
 Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys  
 210 215 220  
 Thr Val Ala Pro Thr Glu Cys Ser  
 225 230

<210> 7  
 <211> 242  
 <212> PRT  
 <213> Human

<400> 7  
 Met Ser Val Pro Thr Met Ala Trp Ala Leu Leu Leu Leu Ser Leu Leu  
 1 5 10 15  
 Thr Gln Gly Thr Gly Ser Trp Ala Gln Ser Ala Leu Thr Gln Pro Arg  
 20 25 30  
 Ser Val Ser Gly Ser Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly  
 35 40 45  
 Thr Ser Ser Asp Ile Gly Gly Tyr Asn Phe Val Ser Trp Tyr Gln Gln  
 50 55 60  
 His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr Asp Ala Thr Lys Arg  
 65 70 75 80  
 Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr  
 85 90 95  
 Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr  
 100 105 110  
 Tyr Cys Cys Ser Tyr Ala Gly Asp Tyr Thr Pro Gly Val Val Phe Gly  
 115 120 125  
 Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser  
 130 135 140  
 Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala  
 145 150 155 160  
 Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val  
 165 170 175  
 Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr  
 180 185 190  
 Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu  
 195 200 205  
 Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln  
 210 215 220  
 Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu  
 225 230 235 240  
 Cys Ser

<210> 8  
 <211> 1431  
 <212> DNA  
 <213> Human

## 08321-110PC2 SEQLIST.txt

```

<400> 8
atggactgga cctggagggt cctctttgtg gtggcagcag ctacaggtgt ccagtcccag 60
gtgcagctgg tgcagtctgg ggctgagggt aagaagcctg ggtcctcggg gaaggtctcc 120
tgcaaggctt ctggaggcac cttcaacagg tatactgtca actgggtgcg acagggccct 180
ggacaagggc ttgagtggat gggaggcatc atccctatct ttggtacagc aaactacgca 240
cagaggttcc agggcagact caccattacc gcggacgaat ccacgagcac agcctacatg 300
gagctgagca gcctgagatc tgatgacacg gccgtgtatt tctgtgagag agagaatctc 360
gataattcgg ggacttatta ttatttctca ggctggttcg acccctgggg ccaggggaacc 420
ctggtcaccg tctcctcagc ctccaccaag ggcccatcgg tcttccccct ggacacctcc 480
tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtaagga ctacttcccc 540
gaaccggtga cgggtgctgt gaactcaggc gccctgacca gcggcgtgca caccttcccc 600
gctgtcctac agtcctcagg actctactcc ctacgagcgc tgggtgaccgt gccctccagc 660
agcttgggca cccagacctt catctgcaac gtgaatcaca agcccagcaa caccaggtg 720
gacaagagag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780
cctgaactcc tggggggacc gtcagtcctc ctcttcccc caaaacccaa ggacacctc 840
atgatctccc ggacccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagacctt 900
gaggtcaagt tcaactggta cgtggacggc gtggagggtg ataatgccaa gacaagccg 960
cgggaggagc agtacaacag cacgtaccgt atggtcagcg tcctcaccgt cctcaccag 1020
gactggctga atggcaagga gtacaagtgc aagggtctcca acaaagccct cccagcccc 1080
atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacacctg 1140
cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1200
ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacactac 1260
aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag caagctcacc 1320
gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1380
ctgcacaacc actacacgca gaagagcctc tccctgtccc cgggtaaatg a 1431

```

```

<210> 9
<211> 476
<212> PRT
<213> Human

```

```

<400> 9
Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
1      5      10      15
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20      25      30
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
35      40      45
Asn Arg Tyr Thr Val Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50      55      60
Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala
65      70      75      80
Gln Arg Phe Gln Gly Arg Leu Thr Ile Thr Ala Asp Glu Ser Thr Ser
85      90      95
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val
100      105      110
Tyr Phe Cys Ala Arg Glu Asn Leu Asp Asn Ser Gly Thr Tyr Tyr Tyr
115      120      125
Phe Ser Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
130      135      140
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
145      150      155      160
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
165      170      175
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
180      185      190
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
195      200      205
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Leu Gly Thr
210      215      220
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
225      230      235      240
Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
245      250      255
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
260      265      270
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

```

## 08321-110PC2 SEQLIST.txt

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
 275 280 285  
 290 295 300  
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
 305 310 315 320  
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
 325 330 335  
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Val  
 340 345 350  
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala  
 355 360 365  
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
 370 375 380  
 Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
 385 390 395 400  
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
 405 410 415  
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
 420 425 430  
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
 435 440 445  
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
 450 455 460  
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 465 470 475

<210> 10  
 <211> 705  
 <212> DNA  
 <213> Human

<400> 10  
 atggaagccc cagctcagct tctcttctct ctgctactct ggctcccaga taccaccgga 60  
 gaaatttgtg tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 120  
 ctgccttgca gggccagtca gactgctagc aggtacttag cctggtagca acagaaacct 180  
 ggccaggctc ccagactcct catctatgat acatccaaca gggccactgg catcccagcc 240  
 aggttcagtg gcagtgggtc tgggacagac ttcactctct ccatcagcag cctggagcct 300  
 gaagattttg cagtttatta ctgtcagcag cgtttcaact ggccgtggac gttcggccaa 360  
 gggaccaagg tggaattcaa acgaactgtg gctgcacat ctgtcttcat cttcccgcca 420  
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 480  
 cccagagagg ccaaagtaca gtggaagggt gataacgccc tccaatcggg taactcccag 540  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 600  
 ctgagcaaa gactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 660  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag 705

<210> 11  
 <211> 1425  
 <212> DNA  
 <213> Human

<400> 11  
 atggagtttg ggctgagctg gctttttctt gtggctattt taaaagggtg ccagtgtgag 60  
 gtgcagctgt tggagtctgg gggaggcttg gtacagcctg gggggtccct gagactctcc 120  
 tgtgcagcct ctggattcac ctttagcaac tatgccatga gctgggtccg ccaggctcca 180  
 gggaaggggc tggagtgggt ctcagctatt agtgctagt gtcatagcac atatttggca 240  
 gactccgtga agggccgggt caccatctcc agagacaatt ccaagaacac gctgtatctg 300  
 caaatgaaca gcctgagagc cgaggacacg gccgtatatt actgtgcaaa agatcgagag 360  
 gttactatga tagttgtact tttgactact ggggccaggg aaccgggtc 420  
 accgtctcct ccgcctccac caagggccca tcggtcttcc ccctggcacc ctctccaag 480  
 agcacctctg ggggcacagc ggccctgggc tgcttggtca aggactactt ccccgaaaccg 540  
 gtgacgggtg cgtggaactc aggcgccttg accagcggcg tgcacacctt cccggctgtc 600  
 ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 660  
 ggcaaccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 720  
 agagttgagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 780  
 ctctggggg gaccgtcagt cttcctcttc ccccaaaac ccaaggacac cctcatgatc 840  
 tcccggacc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 900

## 08321-110PC2 SEQLIST.txt

```

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 960
gagcagtaca acagcacgta ccgtgtgggtc agcgtcctca ccgtcctgca ccaggactgg 1020
ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag ccctcccagc ccccatcgag 1080
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1140
tcccgggagg agatgaccaa gaaccagggtc agcctgacct gcctgggtcaa aggcttctat 1200
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1260
acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggag 1320
aagagcaggt ggcagcaggg gaacgtcttc tcatgtctcg tgatgcatga ggctctgcac 1380
aaccactaca cgcagaagag cctctccctg tccccgggta aatga 1425

```

<210> 12  
 <211> 729  
 <212> DNA  
 <213> Human

```

<400> 12
atgagtgtcc ccaccatggc ctgggctctg ctctctctca gcctctcac tcagggcaca 60
ggatcctggg ctgactctgc cctgactcag cctcgctcag tgtccgggtc tcctggacag 120
tcagtcacca tctcctgcac tgggaaccag agtgatattg gtgggtataa ctttgtctcc 180
tggtagcaac aacacccagg caaagcccc aaactcatga tttatgatgc cactaagcgg 240
ccctcagggg tccctgatcg cttctctggc tccaagtctg gcaacacggc ctccctgacc 300
atctctgggc tccaggctga ggatgaggct gattattact gctgctcata tgcaggcgac 360
tacaccccg gcgtgggttt cggcggaggg accaagtga ccgtcctagg tcagcccaag 420
gctgccccct cggtcactct gttcccgccc tcctctgagg agcttcaagc caacaaggcc 480
acactggtgt gtctcataag tgacttctac ccgggagccg tgacagtggc ctggaaggca 540
gatagcagcc ccgtcaaggc gggagtggag accaccacac cctccaaaca aagcaacaac 600
aagtacgcgg ccagcagcta cctgagcctg acgcctgagc agtgggaagtc ccacagaagc 660
tacagctgcc aggtcacgca tgaaggagc accgtggaga agacagtggc ccctacagaa 720
tgttcatag 729

```

<210> 13  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 13  
 aaacgtacga tggagtttgg gctgagctgg ctt 33

<210> 14  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 14  
 aacgtacgat ggacacactt tgctccacgc tcct 34

<210> 15  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 15  
 aaacgtacga ccatggactg gacctggagg ttcct 35

<210> 16  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

## 08321-110PC2 SEQLIST.txt

<220>  
 <223> Primer  
  
 <400> 16  
 tgctaggggt gttagttttt ttcatgactc atttaccggg ggacagggga 49  
  
 <210> 17  
 <211> 56  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primer, where n is a 5' end of light chain cDNAs  
  
 <221> misc\_feature  
 <222> (1)...(56)  
 <223> n = A,T,C or G  
  
 <400> 17  
 ggtaaatgag tcatgaaaaa aactaacacc cctagcnnnn nnnnnnnnnn nnnnnn 56  
  
 <210> 18  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primer  
  
 <400> 18  
 aaagctagcc taacactctc ccctgttgaa gctc 34  
  
 <210> 19  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primer  
  
 <400> 19  
 aaagctagcc tatgaacatt ctgtaggggc cactgt 36  
  
 <210> 20  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primer  
  
 <400> 20  
 aaatctagac tatgaacatt ctgtaggggc cac 33  
  
 <210> 21  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primer  
  
 <400> 21  
 cctctagatt acagtctggt ctcaccccc 29  
  
 <210> 22

## 08321-110PC2 SEQLIST.txt

<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 23  
cccgggttaa cagaagagtc aatcgatcag aac 33

<210> 23  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 23  
ttaagttaac caagaatagt ccaatga 27

<210> 24  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 24  
tctcgagccc gggactatga agtgcctttt gtac 34